

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: December 11, 2006, 20:06:08 ; Search time 174.137 Seconds
(without alignments)
855.952 Million cell updates/sec

Title: US-10-784-721-9
Perfect score: 1731
Sequence: 1 KRCAGNFDSEERSWYNGR.....SCCGXGLEVLFGQPVVRKXG 326

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*
10: Geneseqp2006s.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------------|--------------------|
| 1 | 1729 | 99.9 | 326 | 10 AEF92390 | Aef92390 Biotinyia |
| 2 | 1691 | 97.7 | 318 | 10 AEF92389 | Aef92389 Fluoresce |
| 3 | 1612 | 93.1 | 304 | 10 AEF10978 | Aef10978 Mouse c-C |
| 4 | 1605 | 92.7 | 304 | 2 AAW05409 | Aaw05409 Mouse Crk |
| 5 | 1605 | 92.7 | 304 | 7 ADE56188 | Ade56188 Rat Prote |
| 6 | 1588 | 91.7 | 304 | 7 ADE56190 | Ade56190 Human Pro |
| 7 | 1588 | 91.7 | 304 | 8 ADJ66607 | Adj66607 CRK prote |

| | | | | | |
|----|-------|------|-----|------------|---------------------|
| 8 | 1588 | 91.7 | 304 | 8 ADR99143 | Adr99143 v-crck aar |
| 9 | 1129 | 65.2 | 256 | 2 AAR85919 | Aar85919 Human GRB |
| 10 | 1058 | 61.1 | 204 | 9 ADY68650 | Ady68650 Human v-C |
| 11 | 917.5 | 53.0 | 303 | 2 AAW42071 | Aaw42071 Human Crk |
| 12 | 917.5 | 53.0 | 303 | 9 ADM08737 | Adm08737 Human pro |
| 13 | 917.5 | 53.0 | 389 | 8 ADP48927 | Adp48927 Human-her |
| 14 | 917.5 | 53.0 | 443 | 8 ADP48921 | Adp48921 Human-yea |
| 15 | 917.5 | 53.0 | 444 | 8 ADP48949 | Adp48949 Human-yea |
| 16 | 917.5 | 53.0 | 455 | 8 ADP48947 | Adp48947 Human-yea |
| 17 | 913.5 | 52.8 | 303 | 2 AAR77439 | Aar77439 Mouse CRK |
| 18 | 905.5 | 52.3 | 447 | 8 ADP48913 | Adp48913 Human-yea |
| 19 | 642.5 | 37.1 | 271 | 4 ABB58271 | Abb58271 Drosophil |
| 20 | 387.5 | 22.4 | 107 | 7 ADN11818 | Adn11818 v-Crk SH2 |
| 21 | 321 | 18.5 | 79 | 2 AAW54313 | Aaw54313 NH2-termi |
| 22 | 257 | 14.8 | 50 | 3 AAB12071 | Aab12071 SH3 domai |
| 23 | 257 | 14.8 | 217 | 2 AAW18063 | Aaw18063 Growth fa |
| 24 | 257 | 14.8 | 217 | 7 ADG14308 | Adg14308 Human Grb |
| 25 | 257 | 14.8 | 217 | 7 ADN95325 | Adn95325 Human BEC |
| 26 | 251 | 14.5 | 50 | 7 ADE84644 | Ade84644 v-crck SH3 |
| 27 | 236 | 13.6 | 211 | 4 ABB62014 | Abb62014 Drosophil |
| 28 | 234.5 | 13.5 | 234 | 8 ADP48915 | Adp48915 Human-yea |
| 29 | 231.5 | 13.4 | 211 | 8 ADP48923 | Adp48923 Human-yea |
| 30 | 231.5 | 13.4 | 212 | 8 ADP48950 | Adp48950 Human-yea |
| 31 | 230 | 13.3 | 211 | 8 ADP48917 | Adp48917 Human-yea |
| 32 | 228 | 13.2 | 158 | 8 ADP48929 | Adp48929 Human-her |
| 33 | 224 | 12.9 | 217 | 2 AAR85918 | Aar85918 Human GRB |
| 34 | 224 | 12.9 | 217 | 2 AAW14004 | Aaw14004 Human GRB |
| 35 | 224 | 12.9 | 217 | 2 AAW42070 | Aaw42070 Growth fa |
| 36 | 224 | 12.9 | 217 | 5 ABB57107 | Abb57107 Mouse isc |
| 37 | 224 | 12.9 | 217 | 7 ADD18644 | Add18644 Human dis |
| 38 | 224 | 12.9 | 217 | 7 ADE56262 | Ade56262 Human pro |
| 39 | 224 | 12.9 | 217 | 7 ADD45298 | Add45298 Human pro |
| 40 | 224 | 12.9 | 217 | 7 ADD45296 | Add45296 Rat Prote |
| 41 | 224 | 12.9 | 217 | 7 ADE58870 | Ade58870 Rat Prote |
| 42 | 224 | 12.9 | 217 | 7 ADE58872 | Ade58872 Human Pro |
| 43 | 224 | 12.9 | 217 | 7 ADE56260 | Ade56260 Rat Prote |
| 44 | 224 | 12.9 | 217 | 8 ADJ66547 | Adj66547 Grb2 prot |
| 45 | 224 | 12.9 | 217 | 8 ABM81927 | Abm81927 Tumour-as |

ALIGNMENTS

RESULT 1
AEF92390
ID AEF92390 standard; protein; 326 AA.

XX
AC AEF92390;
XX
DT 20-APR-2006 (first entry)
XX
DE Biotinylated fluorescein-labeled mouse ABL tyrosine kinase.
XX
KW enzyme; protein engineering; protein kinetics; protein interaction;
KW phosphorylation; dephosphorylation; fluorescence; fusion protein; sensor;
KW Abelson murine leukemia viral oncogene homolog tyrosine kinase;
KW ABL tyrosine kinase; cell signaling.

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OM protein - protein search, using sw model

Run on: December 11, 2006, 20:06:57 ; Search time 196.916 Seconds
(without alignments)
1531.388 Million cell updates/sec

Title: US-10-784-721-9

Perfect score: 1731

Sequence: 1 KRCCAGNFDSEERSWYGR.....SGCGXGLEVLFGQPVKRGXG 326

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|----------------|---------------------|
| 1 | 1612 | 93.1 | 304 | 1 CRK_MOUSE | Q64010 mus musculus |
| 2 | 1612 | 93.1 | 304 | 2 Q5ND51_MOUSE | Q5nd51 m v-crck sar |
| 3 | 1609 | 93.0 | 304 | 2 Q96HJ0_HUMAN | Q96hj0 homo sapien |
| 4 | 1605 | 92.7 | 304 | 1 CRK_RAT | Q63768 rattus norv |
| 5 | 1594 | 92.1 | 304 | 2 Q91VM1_MOUSE | Q91vm1 mus musculus |
| 6 | 1588 | 91.7 | 304 | 1 CRK_HUMAN | P46108 homo sapien |
| 7 | 1379.5 | 79.7 | 305 | 1 CRK_CHICK | Q04929 gallus gall |
| 8 | 1361 | 78.6 | 257 | 2 Q8PE7_MOUSE | Q8pe7 mus musculus |
| 9 | 1357 | 78.4 | 296 | 2 Q6GLF5_XENTR | Q6glf5 xenopus tro |
| 10 | 1353 | 78.2 | 283 | 2 Q920I1_MOUSE | Q920i1 mus musculus |
| 11 | 1315 | 76.0 | 296 | 1 CRK_XENLA | P87378 xenopus lae |
| 12 | 1159 | 67.0 | 223 | 2 Q5ND50_MOUSE | Q5nd50 mus musculus |
| 13 | 1140.5 | 65.9 | 311 | 2 Q6DEM2_BRARE | Q6dem2 brachydanio |
| 14 | 1078 | 62.3 | 239 | 2 Q9QW60_9MURI | Q9qw60 mus sp. grb |
| 15 | 1063.5 | 61.4 | 333 | 2 Q4TDQ2_TETNG | Q4tdq2 tetraodon n |

| | | | | | | |
|----|-------|------|-----|---|--------------|---------------------|
| 16 | 1061 | 61.3 | 204 | 2 | Q8JZR2_MOUSE | Q8jzr2 m crk prote |
| 17 | 1058 | 61.1 | 204 | 2 | Q96GA9_HUMAN | Q96ga9 homo sapien |
| 18 | 1055 | 60.9 | 261 | 2 | Q3TTI0_MOUSE | Q3tti0 mus musculus |
| 19 | 1007 | 58.2 | 254 | 2 | Q6PAB9_XENLA | Q6pab9 xenopus lae |
| 20 | 938 | 54.2 | 302 | 2 | Q66KG8_XENLA | Q66kg8 xenopus lae |
| 21 | 938 | 54.2 | 302 | 2 | Q6NTZ1_XENLA | Q6ntz1 xenopus lae |
| 22 | 925.5 | 53.5 | 305 | 2 | Q6PH06_BRARE | Q6ph06 brachydanio |
| 23 | 917.5 | 53.0 | 303 | 1 | CRKL_HUMAN | P46109 homo sapien |
| 24 | 917.5 | 53.0 | 303 | 2 | Q5UZU2_RAT | Q5uzu2 rattus norv |
| 25 | 913.5 | 52.8 | 303 | 1 | CRKL_MOUSE | P47941 mus musculus |
| 26 | 913.5 | 52.8 | 303 | 2 | Q3TQ18_MOUSE | Q3tq18 mus musculus |
| 27 | 865.5 | 50.0 | 295 | 2 | Q48Z13_TETNG | Q48z13 tetraodon n |
| 28 | 849 | 49.0 | 338 | 2 | Q4SW52_TETNG | Q4sw52 tetraodon n |
| 29 | 836.5 | 48.3 | 249 | 2 | Q4TEX3_TETNG | Q4tex3 tetraodon n |
| 30 | 834.5 | 48.2 | 255 | 2 | Q99059_9RETR | Q99059 avian sarco |
| 31 | 818.5 | 47.3 | 440 | 1 | GAGC_AVISC | P05433 avian sarco |
| 32 | 659.5 | 38.1 | 289 | 2 | Q6P8B4_XENTR | Q6p8b4 xenopus tro |
| 33 | 652.5 | 37.7 | 256 | 2 | Q7QG48_ANOGA | Q7qg48 anopheles g |
| 34 | 642.5 | 37.1 | 271 | 1 | CRK_DROME | Q9XYM0 drosophila |
| 35 | 642.5 | 37.1 | 271 | 2 | Q53XD2_DROME | Q53xd2 drosophila |
| 36 | 591.5 | 34.2 | 253 | 2 | Q9SRW2_DROME | Q9srw2 drosophila |
| 37 | 427 | 24.7 | 82 | 2 | Q3TOV3_MOUSE | Q3tov3 mus musculus |
| 38 | 367.5 | 21.2 | 98 | 2 | Q8RSB8_MOUSE | Q8rsb8 mus musculus |
| 39 | 343 | 19.8 | 279 | 2 | Q9NHC3_CABEL | Q9nhc3 caenorhabdi |
| 40 | 333 | 19.2 | 277 | 2 | Q61AY7_CABER | Q61ay7 caenorhabdi |
| 41 | 257 | 14.8 | 217 | 1 | GRAP_HUMAN | Q13588 homo sapien |
| 42 | 236 | 13.6 | 211 | 1 | DRK_DROME | Q08012 drosophila |
| 43 | 236 | 13.6 | 211 | 1 | DRK_DROSI | Q6YK48 drosophila |
| 44 | 233 | 13.5 | 211 | 2 | Q7PV64_ANOGA | Q7pv64 anopheles g |
| 45 | 229 | 13.2 | 217 | 1 | GRAP_MOUSE | Q9CX99 mus musculus |

ALIGNMENTS

RESULT 1

CRK_MOUSE
ID CRK_MOUSE STANDARD; PRT; 304 AA.
AC Q64010;
DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
DE 01-NOV-1996, sequence version 1.
DT 07-MAR-2006, entry version 51.
DE Proto-oncogene C-crck (P38) (Adapter molecule crk).
GN Names=Crk; Synonyms=Crko;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS CRK-I AND CRK-II).
RC TISSUE=Liver;
RX MEDLINE=94239744; PubMed=8183562;
RA Ogawa S., Toyoshima H., Kozutsumi H., Hagiwara K., Sakai R.,
RA Tanaka T., Hirano N., Mano H., Yazaki Y., Hirai H.;
RT "The C-terminal SH3 domain of the mouse C-Crk protein negatively
regulates tyrosine-phosphorylation of Crk associated p130 in rat 3Y1

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OM protein - protein search, using sw model

Run on: December 11, 2006, 20:12:59 ; Search time 26.8292 Seconds
(without alignments)
1169.124 Million cell updates/sec

Title: US-10-784-721-9

Perfect score: 1731

Sequence: 1 KRGCAGNFDSEERSMYWGR.....SGCGXGLEVLPGQFVRKXG 326

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_80:**

1: pir1:**

2: pir2:**

3: pir3:**

4: pir4:**

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|----------|--------------------|
| 1 | 1612 | 93.1 | 304 | 2 158394 | C-Crk - mouse |
| 2 | 1588 | 91.7 | 304 | 2 A45022 | CRK-II - human |
| 3 | 1379.5 | 79.7 | 305 | 1 A49011 | C-Crk - chicken |
| 4 | 1078 | 62.3 | 239 | 2 A46243 | epidermal growth f |
| 5 | 1052 | 60.8 | 204 | 2 B45022 | CRK-I - human |
| 6 | 917.5 | 53.0 | 303 | 2 S41754 | CRKL protein - hum |
| 7 | 911.5 | 52.7 | 303 | 2 S58352 | SH2/SH3 adaptor pr |
| 8 | 834.5 | 48.2 | 259 | 2 A44988 | transforming prote |
| 9 | 818.5 | 47.3 | 232 | 1 TVFV10 | transforming prote |
| 10 | 216 | 13.6 | 211 | 2 A46444 | SH2-SH3 adaptor pr |
| 11 | 224 | 12.9 | 217 | 2 A43321 | growth factor rece |
| 12 | 224 | 12.9 | 217 | 2 A54688 | modular adaptor Gr |
| 13 | 224 | 12.9 | 217 | 2 S26050 | growth factor rece |

| | | | | | |
|----|-------|------|------|----------|--------------------|
| 14 | 218 | 12.6 | 217 | 2 JT0664 | growth factor rece |
| 15 | 202 | 11.7 | 228 | 2 S25730 | SH2-SH3 protein se |
| 16 | 184 | 10.6 | 1291 | 2 S00666 | 1-phosphatidylinos |
| 17 | 182 | 10.5 | 1097 | 2 T31504 | hypothetical prote |
| 18 | 178 | 10.3 | 1290 | 2 A36466 | 1-phosphatidylinos |
| 19 | 177 | 10.2 | 1290 | 2 A31317 | 1-phosphatidylinos |
| 20 | 172.5 | 10.0 | 839 | 1 TVHVVV | transforming prote |
| 21 | 170 | 9.8 | 816 | 2 T17257 | hypothetical prote |
| 22 | 167 | 9.6 | 844 | 1 TVMSVV | transforming prote |
| 23 | 165 | 9.5 | 1270 | 2 T09194 | adaptor protein in |
| 24 | 164 | 9.5 | 1196 | 2 T14108 | SH3-containing pro |
| 25 | 161 | 9.3 | 1094 | 2 T13053 | dynamn associated |
| 26 | 158.5 | 9.2 | 330 | 2 JE0376 | Grb-2 related adap |
| 27 | 154.5 | 8.9 | 878 | 2 T51940 | gene VAV2 protein |
| 28 | 152.5 | 8.8 | 1011 | 2 T13055 | dynamn associated |
| 29 | 151.5 | 8.8 | 334 | 2 T33836 | hypothetical prote |
| 30 | 151 | 8.7 | 1168 | 1 MWXIC | myosin heavy chain |
| 31 | 150 | 8.7 | 443 | 2 T27877 | hypothetical prote |
| 32 | 150 | 8.7 | 960 | 1 A39651 | discs-large tumor |
| 33 | 149.5 | 8.6 | 639 | 2 T13151 | adaptor protein CM |
| 34 | 148.5 | 8.6 | 1113 | 1 A47106 | myosin heavy chain |
| 35 | 148 | 8.5 | 290 | 2 T42526 | hypothetical prote |
| 36 | 147 | 8.5 | 1044 | 2 S01966 | GTPase-activating |
| 37 | 146.5 | 8.5 | 1038 | 2 JT0663 | ras GTPase-activat |
| 38 | 146 | 8.4 | 946 | 2 T38100 | rho-GTPase-activat |
| 39 | 144.5 | 8.3 | 1047 | 2 A40121 | GTPase-activating |
| 40 | 143.5 | 8.3 | 870 | 2 B40121 | GTPase-activating |
| 41 | 142 | 8.2 | 450 | 2 A41973 | protein-tyrosine k |
| 42 | 141 | 8.1 | 665 | 2 JC7191 | 85K c-Cbl-interact |
| 43 | 139.5 | 8.1 | 1236 | 1 A53970 | 1-phosphatidylinos |
| 44 | 139 | 8.0 | 359 | 2 S27788 | neutrophil oxidase |
| 45 | 139 | 8.0 | 1196 | 2 T23832 | protein-tyrosine k |

ALIGNMENTS

RESULT 1

I58394
C-Crk - mouse
C.Species: Mus sp. (mouse)
C.Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C.Accession: I58394
R.Ogawa, S.; Toyoshima, H.; Kozutsumi, H.; Hagiwara, K.; Sakai, R.; Tanaka, T.; Hirano, N.; Mano, H.; Yazaki, Y.; Hirai, H.
Oncogene 9, 1669-1678, 1994
A>Title: The C-terminal SH3 domain of the mouse c-Crk protein negatively regulates tyrosine-phosphorylation of Crk associated p130 in rat 3Y1 cells.
A.Reference number: I58394; MUID:94239744; PMID:8183562
A.Accession: I58394
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: mRNA
A.Residues: 1-304 <RES>
A.Cross-references: UNIPARC:UPI0000003F6F; GB:S72408; NID:9632866; PIDN:AB30755.1; PID:9632867
C.Genetics:
C.Gene: c-crk

OM protein - protein search, using sw model

Run on: December 11, 2006, 20:06:08 ; Search time 169.863 Seconds
(without alignments)
855.952 Million cell updates/sec

Title: US-10-784-721-8

Perfect score: 1692

Sequence: 1 KRGCAGNFDSEERSWTGCR.....QQNPDEDFSGCGKLEVLFPQ 318

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 segs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database : A_Geneseq.8.*

- 1: geneseqp1980s.*
- 2: geneseqp1990s.*
- 3: geneseqp2000s.*
- 4: geneseqp2001s.*
- 5: geneseqp2002s.*
- 6: geneseqp2003as.*
- 7: geneseqp2003bs.*
- 8: geneseqp2004s.*
- 9: geneseqp2005s.*
- 10: geneseqp2006s.*

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|------------|-------|-------------|--------|-------------|--------------------|
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| 2 | 1691 | 99.9 | 326 | 10 AEF92390 | Aef92390 Biotinyla |
| 3 | 1612 | 95.3 | 304 | 10 AEF10978 | Aef10978 Mouse c-C |
| 4 | 1605 | 94.9 | 304 | 2 AAW05409 | Aaw05409 Mouse Crk |
| 5 | 1605 | 94.9 | 304 | 7 ADE56188 | Ade56188 Rat Prote |
| 6 | 1588 | 93.9 | 304 | 7 ADE56190 | Ade56190 Human Pro |
| 7 | 1588 | 93.9 | 304 | 8 ADJ66607 | Adj66607 CRK prote |

| | | | | | | |
|----|-------|------|-----|---|----------|---------------------|
| 8 | 1588 | 93.9 | 304 | 8 | ADR99143 | Adr99143 V-crck sar |
| 9 | 1129 | 66.7 | 256 | 2 | AAR85919 | Aar85919 Human GRB |
| 10 | 1058 | 62.5 | 204 | 9 | ADY68650 | Ady68650 Human V-C |
| 11 | 917.5 | 54.2 | 303 | 2 | AAW42071 | Aaw42071 Human Crk |
| 12 | 917.5 | 54.2 | 303 | 9 | ADM08737 | Adm08737 Human pro |
| 13 | 917.5 | 54.2 | 389 | 8 | ADP48927 | Adp48927 Human-her |
| 14 | 917.5 | 54.2 | 443 | 8 | ADP48921 | Adp48921 Human-yea |
| 15 | 917.5 | 54.2 | 444 | 8 | ADP48949 | Adp48949 Human-yea |
| 16 | 917.5 | 54.2 | 455 | 8 | ADP48947 | Adp48947 Human-yea |
| 17 | 913.5 | 54.0 | 303 | 2 | AAR77439 | Aar77439 Mouse CRK |
| 18 | 905.5 | 53.5 | 447 | 8 | ADP48913 | Adp48913 Human-yea |
| 19 | 642.5 | 38.0 | 271 | 4 | ABBS8271 | Abbs8271 Drosophil |
| 20 | 387.5 | 22.9 | 107 | 7 | ADN11818 | Adn11818 V-Crk SH2 |
| 21 | 321 | 19.0 | 79 | 2 | AAW54313 | Aaw54313 NH2-termi |
| 22 | 257 | 15.2 | 50 | 3 | AAB12071 | Aab12071 SH3 domai |
| 23 | 257 | 15.2 | 217 | 2 | AAW18063 | Aaw18063 Growth fa |
| 24 | 257 | 15.2 | 217 | 7 | ADG14308 | Adg14308 Human Grb |
| 25 | 257 | 15.2 | 217 | 7 | ADN95325 | Adn95325 Human BEC |
| 26 | 251 | 14.8 | 50 | 7 | ADE84644 | Ade84644 V-crck SH3 |
| 27 | 236 | 13.9 | 211 | 4 | ABB62014 | Abb62014 Drosophil |
| 28 | 234.5 | 13.9 | 234 | 8 | ADP48915 | Adp48915 Human-yea |
| 29 | 231.5 | 13.7 | 211 | 8 | ADP48923 | Adp48923 Human-yea |
| 30 | 231.5 | 13.7 | 212 | 8 | ADP48950 | Adp48950 Human-yea |
| 31 | 230 | 13.6 | 211 | 8 | ADP48917 | Adp48917 Human-yea |
| 32 | 228 | 13.5 | 158 | 8 | ADP48929 | Adp48929 Human-her |
| 33 | 224 | 13.2 | 217 | 2 | AAR85918 | Aar85918 Human GRB |
| 34 | 224 | 13.2 | 217 | 2 | AAW14004 | Aaw14004 Human GRB |
| 35 | 224 | 13.2 | 217 | 2 | AAW42070 | Aaw42070 Growth fa |
| 36 | 224 | 13.2 | 217 | 5 | ABB57107 | Abb57107 Mouse isc |
| 37 | 224 | 13.2 | 217 | 7 | ADD18644 | Add18644 Human dis |
| 38 | 224 | 13.2 | 217 | 7 | ADE56262 | Ade56262 Human pro |
| 39 | 224 | 13.2 | 217 | 7 | ADD45298 | Add45298 Human pro |
| 40 | 224 | 13.2 | 217 | 7 | ADD45296 | Add45296 Rat Prote |
| 41 | 224 | 13.2 | 217 | 7 | ADES8870 | Ade58870 Rat Prote |
| 42 | 224 | 13.2 | 217 | 7 | ADES8872 | Ade58872 Human pro |
| 43 | 224 | 13.2 | 217 | 7 | ADE56260 | Ade56260 Rat Prote |
| 44 | 224 | 13.2 | 217 | 8 | ADJ66547 | Adj66547 Grb2 prot |
| 45 | 224 | 13.2 | 217 | 8 | ABM81927 | Abm81927 Tumout-ag |

ALIGNMENTS

RESULT 1

AEF92389

ID AEF92389 standard; protein; 318 AA.

XX

XX AEF92389;

AC

XX 20-APR-2006 (first entry)

DT Fluorescein-labeled mouse Abl tyrosine kinase.

DE enzyme; protein engineering; protein kinetics; protein interaction;
KW phosphorylation; dephosphorylation; fluorescence; fusion protein; sensor;
KW Abelson murine leukemia viral oncogene homolog tyrosine kinase;
KW Abl tyrosine kinase; cell signaling.

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: December 11, 2006, 20:06:57 ; Search time 192.084 Seconds
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1531.388 Million cell updates/sec

Title: US-10-784-721-8

Perfect score: 1692

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Scoring table: BLOSUM62

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SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|----------------|---------------------|
| 1 | 1612 | 95.3 | 304 | 1 CRK_MOUSE | Q64010 mus musculus |
| 2 | 1612 | 95.3 | 304 | 2 Q5ND51_MOUSE | Q5nd51 m v-crck ear |
| 3 | 1609 | 95.1 | 304 | 2 Q96HJ0_HUMAN | Q96hj0 homo sapien |
| 4 | 1605 | 94.9 | 304 | 1 CRK_RAT | Q63768 rattus norv |
| 5 | 1594 | 94.2 | 304 | 2 Q91VM1_MOUSE | Q91vm1 mus musculus |
| 6 | 1588 | 93.9 | 304 | 1 CRK_HUMAN | P46108 homo sapien |
| 7 | 1379.5 | 81.5 | 305 | 1 CRK_CHICK | Q04929 gallus gall |
| 8 | 1361 | 80.4 | 257 | 2 Q8BPE7_MOUSE | Q8bpe7 mus musculus |
| 9 | 1357 | 80.2 | 296 | 2 Q6GLF5_XENTR | Q6glf5 xenopus tro |
| 10 | 1353 | 80.0 | 283 | 2 Q920I1_MOUSE | Q920i1 mus musculus |
| 11 | 1315 | 77.7 | 296 | 1 CRK_XENLA | P87378 xenopus lae |
| 12 | 1159 | 68.5 | 223 | 2 Q5ND50_MOUSE | Q5nd50 mus musculus |
| 13 | 1140.5 | 67.4 | 311 | 2 Q6DEM2_BRARE | Q6dem2 brachydanio |
| 14 | 1078 | 63.7 | 239 | 2 Q9QW60_9MURI | Q9qw60 mus sp. grb |
| 15 | 1063.5 | 62.9 | 333 | 2 Q4TDQ2_TETNG | Q4tdq2 tetraodon n |

| | | | | | |
|----|-------|------|-----|----------------|--------------------|
| 16 | 1061 | 62.7 | 204 | 2 Q8JZR2_MOUSE | Q8jzr2 m crk prote |
| 17 | 1058 | 62.5 | 204 | 2 Q96GA9_HUMAN | Q96ga9 homo sapien |
| 18 | 1055 | 62.4 | 261 | 2 Q3TTI0_MOUSE | Q3ttio mus musculu |
| 19 | 1007 | 59.5 | 254 | 2 Q6PAB9_XENLA | Q6pab9 xenopus lae |
| 20 | 938 | 55.4 | 302 | 2 Q66KG8_XENLA | Q66kg8 xenopus lae |
| 21 | 938 | 55.4 | 302 | 2 Q6NTZ1_XENLA | Q6ntz1 xenopus lae |
| 22 | 925.5 | 54.7 | 305 | 2 Q6PH06_BRARE | Q6ph06 brachydanio |
| 23 | 917.5 | 54.2 | 303 | 1 CRKL_HUMAN | P46109 homo sapien |
| 24 | 917.5 | 54.2 | 303 | 2 Q5U2U2_RAT | Q5u2u2 rattus norv |
| 25 | 913.5 | 54.0 | 303 | 1 CRKL_MOUSE | P47941 mus musculu |
| 26 | 913.5 | 54.0 | 303 | 2 Q3TQ18_MOUSE | Q3tq18 mus musculu |
| 27 | 865.5 | 51.2 | 295 | 2 Q4RZ13_TETNG | Q4rz13 tetraodon n |
| 28 | 849 | 50.2 | 338 | 2 Q4SW52_TETNG | Q4sw52 tetraodon n |
| 29 | 836.5 | 49.4 | 249 | 2 Q4TEX3_TETNG | Q4tex3 tetraodon n |
| 30 | 834.5 | 49.3 | 255 | 2 Q99059_9RETR | Q99059 avian sarco |
| 31 | 818.5 | 48.4 | 440 | 1 GAGC_AVIC | P05433 avian sarco |
| 32 | 659.5 | 39.0 | 289 | 2 Q6P8B4_XENTR | Q6p8b4 xenopus tro |
| 33 | 652.5 | 38.6 | 256 | 2 Q7Q848_ANOGA | Q7q848 anopheles g |
| 34 | 642.5 | 38.0 | 271 | 1 CRK_DROME | Q9xymo drosophila |
| 35 | 642.5 | 38.0 | 271 | 2 Q53XD2_DROME | Q53xd2 drosophila |
| 36 | 591.5 | 35.0 | 253 | 2 Q95RW2_DROME | Q95rw2 drosophila |
| 37 | 427 | 25.2 | 82 | 2 Q3TOV3_MOUSE | Q3tov3 mus musculu |
| 38 | 367.5 | 21.7 | 98 | 2 Q8RSB8_MOUSE | Q8rsb8 mus musculu |
| 39 | 343 | 20.3 | 279 | 2 Q9NHC3_CABEL | Q9nhc3 caenorhabdi |
| 40 | 333 | 19.7 | 277 | 2 Q61AY7_CABBR | Q61ay7 caenorhabdi |
| 41 | 257 | 15.2 | 217 | 1 GRAP_HUMAN | Q13588 homo sapien |
| 42 | 236 | 13.9 | 211 | 1 DRK_DROME | Q08012 drosophila |
| 43 | 236 | 13.9 | 211 | 1 DRK_DROSI | Q5ytaa8 drosophila |
| 44 | 233 | 13.8 | 211 | 2 Q7PV64_ANOGA | Q7pv64 anopheles g |
| 45 | 229 | 13.5 | 217 | 1 GRAP_MOUSE | Q9cx99 mus musculu |

ALIGNMENTS

RESULT 1

CRK_MOUSE
ID CRK_MOUSE STANDARD; PRT; 304 AA.
AC Q64010;
DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1996, sequence version 1.
DT 07-MAR-2006, entry version 51.
DE Proto-oncogene C-crck (P38) (adapter molecule crk).
GN Names=Crk; Synonyms=Crko;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS CRK-I AND CRK-II).
RC TISSUE=Liver;
RA MEDLINE=94239744; PubMed=8183562;
RA Ogawa S., Toyoshima H., Kozutsumi H., Hagiwara K., Sakai R.,
RA Tanaka T., Hirano N., Mano H., Yazaki Y., Hirai H.;
RT "The C-terminal SH3 domain of the mouse c-Crk protein negatively
regulates tyrosine-phosphorylation of Crk associated p130 in rat 3Y1

OM protein - protein search, using sw model

Run on: December 11, 2006, 20:12:59 ; Search time 26.1708 Seconds
(without alignments)
1169.124 Million cell updates/sec

Title: US-10-784-721-8

Perfect score: 1692

Sequence: 1 KRQAGNFDSEERSWYGR.....QQNPDEDFGCGXGLEVLQ 318

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----------|--------------------|
| 1 | 1612 | 95.3 | 304 | 2 158394 | C-Crk - mouse |
| 2 | 1588 | 93.9 | 304 | 2 A45022 | CRK-II - human |
| 3 | 1379.5 | 81.5 | 305 | 1 A49011 | C-Crk - chicken |
| 4 | 1078 | 63.7 | 239 | 2 A46243 | epidermal growth f |
| 5 | 1052 | 62.2 | 204 | 2 B45022 | CRK-I - human |
| 6 | 917.5 | 54.2 | 303 | 2 S41754 | CRKL protein - hum |
| 7 | 911.5 | 53.9 | 303 | 2 S58352 | SH2/SH3 adaptor pr |
| 8 | 834.5 | 49.3 | 259 | 2 A44988 | transforming prote |
| 9 | 818.5 | 48.4 | 232 | 1 TVFV10 | transforming prote |
| 10 | 236 | 13.9 | 211 | 2 A46444 | SH2-SH3 adaptor pr |
| 11 | 224 | 13.2 | 217 | 2 A43321 | growth factor rece |
| 12 | 224 | 13.2 | 217 | 2 A54688 | modular adaptor Gr |
| 13 | 224 | 13.2 | 217 | 2 S26050 | growth factor rece |

| | | | | | |
|----|-------|------|------|----------|---------------------|
| 14 | 218 | 12.9 | 217 | 2 JT0664 | growth factor rece |
| 15 | 202 | 11.9 | 228 | 2 S25730 | SH2-SH3 protein se |
| 16 | 184 | 10.9 | 1291 | 2 S00666 | 1-phosphatidylinos |
| 17 | 182 | 10.8 | 1290 | 2 T31504 | hypothetical prote |
| 18 | 178 | 10.5 | 1290 | 2 A36466 | 1-phosphatidylinos |
| 19 | 177 | 10.5 | 1290 | 2 A31317 | 1-phosphatidylinos |
| 20 | 172.5 | 10.2 | 839 | 1 TVROVV | transforming prote |
| 21 | 170 | 10.0 | 816 | 2 T17257 | hypothetical prote |
| 22 | 167 | 9.9 | 844 | 1 TVMSVV | transforming prote |
| 23 | 165 | 9.8 | 1270 | 2 T09194 | adaptor protein in |
| 24 | 164 | 9.7 | 1196 | 2 T14108 | SH3-containing pro |
| 25 | 161 | 9.5 | 1094 | 2 T13053 | dynamain associated |
| 26 | 158.5 | 9.4 | 330 | 2 JE0376 | Grb-2 related adap |
| 27 | 154.5 | 9.1 | 878 | 2 I51940 | gene VAV2 protein |
| 28 | 152.5 | 9.0 | 1011 | 2 T13055 | dynamain associated |
| 29 | 151.5 | 9.0 | 334 | 2 T33836 | hypothetical prote |
| 30 | 151 | 8.9 | 1168 | 1 MWAXIC | myosin heavy chain |
| 31 | 150 | 8.9 | 960 | 1 A39651 | discs-large tumor |
| 32 | 149 | 8.8 | 639 | 2 T13151 | adaptor protein CM |
| 33 | 148.5 | 8.8 | 1113 | 1 A47106 | myosin heavy chain |
| 34 | 148 | 8.7 | 290 | 2 T42526 | hypothetical prote |
| 35 | 146 | 8.7 | 443 | 2 T27877 | hypothetical prote |
| 36 | 147 | 8.7 | 1044 | 2 S01966 | GTPase-activating |
| 37 | 146.5 | 8.7 | 1038 | 2 JT0663 | ras GTPase-activat |
| 38 | 146 | 8.6 | 946 | 2 I38100 | rho-GTPase-activat |
| 39 | 144.5 | 8.5 | 1047 | 2 A40121 | GTPase-activating |
| 40 | 143.5 | 8.5 | 870 | 2 B40121 | GTPase-activating |
| 41 | 142 | 8.4 | 450 | 2 A41973 | protein-tyrosine k |
| 42 | 141 | 8.3 | 665 | 2 JC7191 | 85k c-Cbl-interact |
| 43 | 139.5 | 8.2 | 1236 | 1 A53970 | 1-phosphatidylinos |
| 44 | 139 | 8.2 | 359 | 2 S27788 | neutrophil oxidase |
| 45 | 139 | 8.2 | 1196 | 2 T23832 | protein-tyrosine k |

ALIGNMENTS

RESULT 1

158394

C-Crk - mouse

C:Species: Mus sp. (mouse)

C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999

C:Accession: 158394

R.Ogawa, S.; Toyoshima, H.; Kozutsumi, H.; Hagiwara, K.; Sakai, R.; Tanaka, T.;

Hirano, N.; Mano, H.; Yazaki, Y.; Hirai, H.

Oncogene 9, 1669-1678, 1994

A>Title: The C-terminal SH3 domain of the mouse c-Crk protein negatively
regulates tyrosine-phosphorylation of Crk associated p130 in rat 3Y1 cells.

A:Reference number: 158394; MUID:94239744; PMID:8183562

A:Accession: 158394

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-304 <RES>

A:Cross-references: UNIPARC:UPI0000003F6F; GB:S72408; NID:g632866;

PIDN:AB30755.1; PID:g632867

C:Genetics:

A:Gene: c-crk